



Seq\_listing\_US\_korrigiert141102.txt  
SEQUENCE LISTING

<110> Forschungszentrum Juelich GmbH; Marina Vrlijc et al.

<120> Process for the microbial production of amino acids by boosted activity of export carriers

<130> 1

<140> US/09/105,117 PCT/DE96/02485

<141> 1998-06-17

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 2374

<212> DNA

<213> Corynebacterium glutamicum

<220> (LysE)

<221> gene

<222> CDS (1016)..(1726)

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gtctgtgagt ctagctagag atctagattc caggcgccat cgttgccaat acatcggtgt 180

gtcaatgggt atctcatcga ggaggatcac ttctcctgct ttttagcatgg gagcagctt 240

ggtttcggga agaagtcccc aaccaaggcc tcggcgaatt gcctcaccaa aaccttccgc 300

cgacgggaca atggatacgc gcctgcgccc cacaggacca tcgacgcgcc cgtccaggc 360

acggcttga agcacatctt tgggaccgaa gcgttaagacg ggcacatcgacg cccaatctag 420

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ggttccaagt tctactactt cacatcccgc cacgggatta gcttcacggg ttaccgctcc 540

taaaacatct ccacgcccga gcaaggataa tgtgtgcgct tcacatccca agcgcagcgt 600

gagcgttgct ccaccccaag aagctacctc gttgaacacg ggagggaaacc atgtggatag 660

cgaatctgcg ttgatggcga tggtaacgg gatttcagca aggcgtccag atagttgcgc 720

tttagttct gcttgcagca acaccatttt ccgcgtcgct tgcacaagga cttcacccgc 780

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agctttaacg cgctgactca ccgcccgggg ggaaatggaa agggctaagg aggcgccttc 900

gaagctgcct tcacatga ttgagagcaa agtgtccagt tgaatgggt tcatgaagct 960

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tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga att 1114  
 Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile  
 20 25 30

aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct gac 1162  
 Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp  
 35 40 45

gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc aat 1210  
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 50 55 60 65

gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct tac 1258  
 Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Ile Ala Tyr  
 70 75 80

ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac aag 1306  
 Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys  
 85 90 95

gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc gat 1354  
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 100 105 110

gac acg cct ttg ggc ggt tcg gcg gtg gcc act gac acg cgc aac cgg 1402  
 Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg  
 115 120 125

gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag ccc 1450  
 Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro  
 130 135 140 145

atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat ttg 1498  
 Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu  
 150 155 160

gac gcg ttt gtg ttt atc ggc ggc gtc ggc gcg caa tac ggc gac acc 1546  
 Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr  
 165 170 175

gga cgg tgg att ttc gcc gct ggc gcg ttc gcg gca agc ctg atc tgg 1594  
 Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp  
 180 185 190

ttc ccg ctg gtg ggt ttc ggc gca gca gca ttg tca cgc ccg ctg tcc 1642  
 Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser  
 195 200 205

agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg atg 1690  
 Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met  
 210 215 220 225

acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag ttttcgcggg 1736  
 Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly  
 230 235

ttttgaaatc ggtggccttc gcccaaatgt tgatgccggc gtcgtggaa atctcatcga 1796

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tcgcctccaa ctcggcgtaa gaaaactcca agttgttag tgaatcaagg ctgtgtcca 1856  
gctgctcaac tgacgaagca ccaatcaatg cactggtcac ggtatccgcg ccgtactctc 1916  
cttgctcgcg cagcacccat gcaagcgcca tctgcgcaag tgactgcccg cgttcctggg 1976  
cgatgtcatt gagcttgcg accatatcaa tattgttac gttcaacatg ccctcagaca 2036  
gggacttacc ctggctggcg cgggAACCT ctggaattcc atcgagatat ttgtccgtga 2096  
gcagggccctg cgcaagtggt gagaaagcaa tgacgccaag accattgttgcagact 2156  
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<220> (LysE)

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20 25 30  
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser  
35 40 45  
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser  
50 55 60  
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala  
65 70 75 80  
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn  
85 90 95  
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro  
100 105 110  
Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn  
115 120 125  
Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys  
130 135 140  
Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr  
145 150 155 160  
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp  
165 170 175

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Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile  
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 Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu  
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 Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val  
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tct gga aag gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc 97  
 Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu  
 20 25 30

aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg 145  
 Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu  
 35 40 45

att cat cag cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg 193  
 Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro  
 50 55 60

ggc gat gac ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt 241  
 Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu  
 65 70 75 80

ggc gtc att gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa 289  
 Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys  
 85 90 95

tat ctc gat gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc 337  
 Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser  
 100 105 110

ctg tct gag ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag 385  
 Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys  
 115 120 125

ctc aat gac atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg 433

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Leu	Ala	Trp	Val	Leu	Arg	Glu	Gln	Gly	Glu	Tyr	Gly	Ala	Asp	Thr	Val	
145				150					155			160				
acc	agt	gca	ttg	att	ggt	gct	tcg	tca	gtt	gag	cag	ctg	gac	aac	agc	529
Thr	Ser	Ala	Leu	Ile	Gly	Ala	Ser	Ser	Val	Glu	Gln	Leu	Asp	Asn	Ser	
				165					170			175				
ctt	gat	tca	ctc	aac	aac	ttg	gag	ttt	tct	gac	gcc	gag	ttg	gag	gcg	577
Leu	Asp	Ser	Leu	Asn	Asn	Leu	Glu	Phe	Ser	Asp	Ala	Glu	Leu	Glu	Ala	
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Ile	Asp	Glu	Ile	Ser	His	Asp	Ala	Gly	Ile	Asn	Ile	Trp	Ala	Lys	Ala	
				195			200			205						
acc	gat	tcc	aaa	acc	cgc	gaa	aac	taa	cccatcaaca	tcagttgtat						672
Thr	Asp	Ser	Lys	Thr	Arg	Glu	Asn									
			210		215											
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tgccatcaac	atgggcttta	cccaaaccgg	ctgcttatcg	acgctcacct	ccacccgcac											972
ccggttgcgc	gtgtcagtgg	ccaccgcga	accgcacaaa	ggcgtgtcat	cgggcacggt											1032
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tgtaatgaag	atttccatga	tcaccatcg	gacctatgga	agtacttaag	taaaatgatt											1392
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ttg	ctc	tca	atc	att	gat	gaa	ggc	agc	ttc	gaa	ggc	gcc	tcc	tta	gcc	1492
Leu	Leu	Ser	Ile	Ile	Asp	Glu	Gly	Ser	Phe	Glu	Gly	Ala	Ser	Leu	Ala	
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Leu	Ser	Ile	Ser	Pro	Ser	Ala	Val	Ser	Gln	Arg	Val	Lys	Ala	Leu	Glu	
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cat	cac	gtg	ggt	cga	gtg	ttg	gta	tcg	cgc	acc	caa	ccg	gcc	aaa	gca	
His	His	Val	Gly	Arg	Val	Leu	Val	Ser	Arg	Thr	Gln	Pro	Ala	Lys	Ala	
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275 280 285	
ctg caa gca gaa act aaa gca caa cta tct gga cgc ctt gct gaa atc	1684
Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu Ala Glu Ile	
290 295 300 305	
ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca tgg ttt cct	1732
Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr Trp Phe Pro	
310 315 320	
ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg ctc acg ctg	1780
Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr Leu Thr Leu	
325 330 335	
cgc ttg gaa gat gaa gca cac aca tta tcc ttg ctg cgg cgt gga gat	1828
Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg Arg Gly Asp	
340 345 350	
gtt tta gga gca gta acc cgt gaa gct aat ccc gtg gca gga tgg gaa	1876
Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala Gly Cys Glu	
355 360 365	
gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca acc ccc tca	1924
Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala Thr Pro Ser	
370 375 380 385	
ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg gct gca atg	1972
Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp Ala Ala Met	
390 395 400	
ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac cgt gac ctg	2020
Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp Arg Asp Leu	
405 410 415	
gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta tcc att gtc	2068
Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val Ser Ile Val	
420 425 430	
ccg tcg gca gaa ggt ttt ggt gag gca att cgc cga ggc ctt ggt tgg	2116
Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly Leu Gly Trp	
435 440 445	
gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa gca gga gaa	2164
Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys Ala Gly Glu	
450 455 460 465	
gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg tat tgg caa	2212
Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met Tyr Trp Gln	
470 475 480 485	
cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca gac gcc gtc	2260
Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr Asp Ala Val	
485 490 495	
gtt gat gca gca atc gag gga ttg cgg cct tag ttacttctga aaaggttcag	2313
Val Asp Ala Ala Ile Glu Gly Leu Arg Pro	
500 505	
ggttttcac ttcttcgccc gcaggaattt ggccaggcag agtaaacacct tcagcaatg	2373
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<213> Corynebacterium glutamicum  
<220> (orf3)

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35 40 45  
Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro  
50 55 60  
Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu  
65 70 75 80  
Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys  
85 90 95  
Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser  
100 105 110  
Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys  
115 120 125  
Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala  
130 135 140  
Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val  
145 150 155 160  
Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser  
165 170 175  
Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala  
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195 200 205  
Thr Asp Ser Lys Thr Arg Glu Asn  
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<210> 5  
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<213> Corynebacterium glutamicum  
<220> (LysG)

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 35 40 45

Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val  
 50 55 60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln  
 65 70 75 80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala  
 85 90 95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser  
 100 105 110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr  
 115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu  
 130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg  
 145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp  
 165 170 175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys  
 180 185 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val  
 195 200 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu  
 210 215 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala  
 225 230 235 240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro  
 245 250 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser  
 260 265 270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu  
 275 280 285

Arg Pro  
 290